

SEQUENCE LISTING

<110> Chadwick, Brian Paul
Frischauf, Anna-Maria

<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
POLYPEPTIDES AND NUCLEIC ACIDS

<130> 9598-066

<140> 09/240,639

<141> 1999-01-29

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 2762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(1599)

<400> 1

```
gtggggtcgt atccccggg tggaggccgg ggtggcgccg gccggggcgg gggagcccaa 60
aagaccggct gccgcctgct ccccgga aaa gggcactcgt ctccgtgggt gtggcggagc 120
gcgcgggtgca tgggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttccaga 180
aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaa g atg aga 237
Met Arg
1
aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
5 10 15
ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
20 25 30
cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
35 40 45 50
cgg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
55 60 65
gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
70 75 80
```

act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
tct gcc tat gct gat gtt gaa aag agc gct cag gga atc cgg gaa	621
Ser Ala Tyr Ala Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	
gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag	957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln	
230 235 240	
gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc	1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr	
245 250 255	
tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca	1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Met Ser Ala	
260 265 270	
cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga	1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Pro Ala Lys Asp Gly	
275 280 285 290	
aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg	1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp	
295 300 305	

gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca 1197
 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
 310 315 320

agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac 1245
 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
 325 330 335

aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc 1293
 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
 340 345 350

tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag 1341
 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
 355 360 365 370

aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac 1389
 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
 375 380 385

gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc 1437
 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
 390 395 400

atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc 1485
 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
 405 410 415

agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc 1533
 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
 420 425 430

agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga 1581
 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
 435 440 445 450

cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag 1629
 Gln Lys Ser Pro Ala Ser
 455

cagtgtctgt gtgtctgcat aaaccctcct gtccctggacg tgacttcac ctgaggagcc 1689

acagcacagg ccgtgtcggc actttctgca cactggctct gggacttgca gaaggctcgg 1749

tgctgcctg gcacagcctt cttccagtca catctggcca gagggctgtc tggacctggg 1809

cctgtctcaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac 1869

aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catccccatg ccccgctccg 1929

ggggctgtgg ctgctgtctgt gcattgccc gcgatgggag tcttgtctcc cagcctgtca 1989

gtttctccc cagggcagag ctccccttcc tgcaagagtc tgggaggcgg tgcaggctgt 2049

cctggctgct ctggggagc cgagggacag ccataacacc cccgggacag taggtctggg 2109

cggcaccact gggaactctg gacttgagtg tgtttgctct tccctgggta tgaatgtgtg 2169

agttcaccca gaggcctgct ctcctcacac attgtgtggt ttgggggttaa tgatggaggg 2229
 agacacctct tcatagacgg caggtgccca cctttcaggg agtctcccag catgggcgga 2289
 tgccgggcat gagctgctgt aaactatttg tggctgtgct gcttgagtga cgtctctgtc 2349
 gtgtgggtgc caagtgttg tgtagaaact gtgttctgag cccccttttc tggacaccaa 2409
 ctgtgtcctg tgaatgtatc gctactgtga gctgttcccc cctagccagg gccatgtctt 2469
 aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctcggtgtct 2529
 cgggccacca tccgccacc tcgggctgac ccacacctct ccatggacag tgtgagcccc 2589
 gggccgtgca tctgtctcag tgtggcgtca gtgtcggggc tgagcccctt gagctgtctt 2649
 agtgaatgta cagtgcctgg cacgagctga acctcatgtt ttccactccc aataaaagg 2709
 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2762

<210> 2

<211> 456

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
 1 5 10 15
 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
 20 25 30
 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
 35 40 45
 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
 50 55 60
 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
 65 70 75 80
 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
 85 90 95
 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
 100 105 110
 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
 115 120 125
 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
 130 135 140
 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
 145 150 155 160

Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
 165 170 175
 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
 180 185 190
 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
 195 200 205
 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
 210 215 220
 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
 225 230 235 240
 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
 245 250 255
 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
 260 265 270
 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
 275 280 285
 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
 290 295 300
 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
 305 310 315 320
 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
 325 330 335
 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
 340 345 350
 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
 355 360 365
 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
 370 375 380
 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
 385 390 395 400
 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
 405 410 415
 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
 420 425 430
 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
 435 440 445
 Asn Arg Gln Lys Ser Pro Ala Ser
 450 455

```
<400> 3
accacacgcgt ctggccgcgg gccgcctctg cggcagcgct agtcgccttc tccgaatcgg 60
```

gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac 592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
155 160 165 170

ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
tggttt att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
tggttt cac atg tggtgtg cac ccg cat gga gtg gaa acc acg ggt gcc ctg	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
gac tta ggt ggt gcc tcc acc caa ata tcc ttc gtg gca gga gag aag	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	
atg gat ctg aac acc agc gac atc atg cag gtg tcc ctg tat ggc tac	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	
235 240 245 250	
gta tac acg ctc tac aca cac agc ttc cag tgc tat ggc cgg aat gag	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	
255 260 265	
gct gag aag aag ttt ctg gca atg ctc ctg cag aat tct cct acc aaa	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
aac cat ctc acc aat ccc tgt tac cct cgg gat tat agc atc agc ttc	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
acc atg ggc cat gta ttt gat agc ctg tgc act gtg gac cag agg cca	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
gaa agt tat aac ccc aat gat gtc atc act ttt gaa gga act ggg gac	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	
cca tct ctg tgt aag gag aag gtg gct tcc ata ttt gac ttc aaa gct	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
tgc cat gat caa gaa acc tgt tct ttt gat ggg gtt tat cag cca aag	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Thr Gln Pro Lys	
350 355 360	
att aaa ggg cca ttt gtg gct ttt gca gga ttc tac tac aca gcc agt	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Thr Thr Ala Ser	
365 370 375	
gct tta aat ctt tca ggt agc ttt tcc ctg gac acc ttc aac tcc agc	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Thr Phe Asn Ser Ser	
380 385 390	

acc tgg aat ttc tgc tca cag aat tgg agt cag ctc cca ctg ctg ctc 1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu
395 400 405 410

ccc aaa ttt gat gag gta tat gcc cgc tct tac tgc ttc tca gcc aac 1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn
415 420 425

tac atc tac cac ttg ttt gtg aac ggt tac aaa ttc aca gag gag act 1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Thr
430 435 440

tgg ccc caa ata cac ttt gaa aaa gaa gtg ggg aat agc agc ata gcc 1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala
445 450 455

tgg tct ctt ggc tac atg ctc agc ctg acc aac cag atc cca gct gaa 1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
460 465 470

agc cct ctg atc cgt ctg ccc ata gaa cca cct gtc ttt gtg ggc acc 1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
475 480 485 490

ctc gct ttc ttc aca gtg gca gcc ttg ctg tgt ctg gca ttt ctt gca 1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
495 500 505

tac ctg tgt tca gca acc aga aga aag agg cac tcc gag cat gcc ttt 1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
510 515 520

gac cat gca gtg gat tct gac tgagccttca aagcagctcc tggagtccaa 1699
Asp His Ala Val Asp Ser Asp
525

tggtctgctta gagtcagcct gggtggcacc aggcaatgca ggtgaagtgg ctgccttcag 1759

gaaatacaac taactaaaat caaacaccta ggtcacgtgc ctctcaaata ctgatttctg 1819

ccacagcacc tcttgaggca tcccttggtc attctgtgca tattgttctt cagagacctc 1879

actaccaca tgctgatcta ttggggaaca gagaagagac aggcaccataa ggtcaggctc 1939

tttatattaa gtccccaga ggaagagtaa gttgagaagg tatcagttta atgttgaaga 1999

attgacctca gggctcagtt tccatttccc tccctcagta ttcttctctg caagataccc 2059

attaagcatt tcgccaatca gaatctcatt ttatagtttt tccatttggt cttaaactaa 2119

gactttcttg tagcaatctc gtaagcagtg aacccctca gatcagtaga atatagtatc 2179

tgggggagaa gacttacttc cttcagggca gcagccacag ccaggcttct gtcatacagg 2239

tagatcccca agcacagaga cataaaaaag gtctcccaga aaactataga ccattctcca 2299

agtgaattc ccacttaggg ctctgggtcac tagattgcaa cctgtgtgtt tgtcatcctc 2359

ctcatctcac cattgtattg ctatgccctc ccataaaaaac acattgatcc ctagcaagat 2419
tattgcattc cagattttac tgcctttgct aggcttttgc ttagcaaaagg gctgactttc 2479
cattgttacc atgggtgtata tatttttgc accattccca caagtatact tgatgttgtc 2539
atagaacgaa catcctactc tatgatttac taaccaatta ctttccaga tcatagacct 2599
ctctgcatag tagtcatagg tcttgacttt ggggaaagaa aaggaagctg caggaatatt 2659
tatctccaaa gtcgaatgag aaagaactcc agcaaatcca atggctacaa actaaaaatc 2719
agcattattt catattgctg tttcttagct gaatatggaa taaagaacta ttattttatt 2779
ttgaaaaaaa aaaaaaaa 2797

<210> 4
<211> 529
<212> PRT
<213> Homo sapiens

<400> 4
Met Phe Thr Val Leu Thr Arg Gln Pro Cys Glu Gln Ala Gly Leu Lys
1 5 10 15
Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala Leu Val Val Leu Leu Val
20 25 30
Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
35 40 45
Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
50 55 60
Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
65 70 75 80
Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
85 90 95
Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
100 105 110
Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
115 120 125
His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
130 135 140
Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu Val Leu Glu Ser Ile
145 150 155 160
Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
165 170 175
Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
180 185 190

Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp His Met Trp Val His
 195 200 205
 Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp Leu Gly Gly Ala Ser
 210 215 220
 Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met Asp Leu Asn Thr Ser
 225 230 235 240
 Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val Tyr Thr Leu Tyr Thr
 245 250 255
 His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala Glu Lys Lys Phe Leu
 260 265 270
 Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn His Leu Thr Asn Pro
 275 280 285
 Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr Met Gly His Val Phe
 290 295 300
 Asp Ser Leu Cys Thr Val Asp Gln Arg Pro Glu Ser Tyr Asn Pro Asn
 305 310 315 320
 Asp Val Ile Thr Phe Glu Gly Thr Gly Asp Pro Ser Leu Cys Lys Glu
 325 330 335
 Lys Val Ala Ser Ile Phe Asp Phe Lys Ala Cys His Asp Gln Glu Thr
 340 345 350
 Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys Ile Lys Gly Pro Phe Val
 355 360 365
 Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser Ala Leu Asn Leu Ser Gly
 370 375 380
 Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser Thr Trp Asn Phe Cys Ser
 385 390 395 400
 Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu Pro Lys Phe Asp Glu Val
 405 410 415
 Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn Tyr Ile Tyr His Leu Phe
 420 425 430
 Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr Trp Pro Gln Ile His Phe
 435 440 445
 Glu Lys Glu Val Gly Asn Ser Ser Ile Ala Trp Ser Leu Gly Tyr Met
 450 455 460
 Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu Ser Pro Leu Ile Arg Leu
 465 470 475 480
 Pro Ile Glu Pro Pro Val Phe Val Gly Thr Leu Ala Phe Phe Thr Val
 485 490 495

Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala Tyr Leu Cys Ser Ala Thr
500 505 510

Arg Arg Lys Arg His Ser Glu His Ala Phe Asp His Ala Val Asp Ser
515 520 525

Asp

<210> 5

<211> 1998

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (247) .. (1530)

<400> 5

gcgcgcgcgt tttccttggt cctgggtcaac aaagaaatgt ggagtgtctt ggctgaatcc 60

tcatacagac aagatcatta tgggtgctgtt aggtaggact tgtatccaga tgtaagggtg 120

aaaaagtgat ataataaagg aaccaaggag aaaattcaga aggaaagaaa aaattgcctc 180

tgcaggtgtg cgagcaggat tgcttctgca acaaaagcct ccaccagccc acatcttggg 240

aaaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta 288

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val

1

5

10

tcc tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt 336

Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe

15

20

25

30

gag ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc 384

Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser

35

40

45

acc ttg tat gga att atg ttt gat gca ggg agc act gga act cga att 432

Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile

50

55

60

cat gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta 480

His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu

65

70

75

gaa ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta 528

Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val

80

85

90

gat caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg 576

Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val

95

100

105

110

gcc aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc	624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val	
115 120 125	
cta aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag	672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys	
130 135 140	
gct ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg	720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu	
145 150 155	
gta cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata	768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile	
160 165 170	
tta gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac	816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His	
175 180 185 190	
aga cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa	864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln	
195 200 205	
atc acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg	912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg	
210 215 220	
ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat	960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr	
225 230 235	
aca cat agt tac ttg gga ttt gga ttg aaa gct gca aga cta gca acc	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	
ctg gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	
255 260 265 270	
gcc tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	
275 280 285	
aaa tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc	1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	
290 295 300	
tgc tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	
305 310 315	
gag gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	
320 325 330	

cga gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta 1296
 Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu
 335 340 345 350

aaa gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg 1344
 Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu
 355 360 365

gaa aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac 1392
 Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
 370 375 380

atc aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc 1440
 Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val
 385 390 395

tta cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg 1488
 Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
 400 405 410

ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat 1530
 Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
 415 420 425

tgaggccacg tactctcttg gagacctgca ttgccaaca cctttttaag gggaggagag 1590

agcacttagt ttctgaacta gtctgggaca tcctggactt gagcctagag atttaggttt 1650

aattaatttt acacatctaa tgtgaactgc tgcctaacca ctcaagagta cacagctggc 1710

accagagcat cacagagagc cctgtgagcc aaaaagtata gttttggaac ttaaccttgg 1770

agtgagagcc cagggacagg tccttggaata ccaagaaaa atcgatttc aaccttttga 1830

gtgcctcatt ccaactgaata tttaaatttt cctcttaaat ggtaaaactga cttattgcaa 1890

tccaagacc catcaatata agtatatttt tcctccctat acagtgcctt gccacccttt 1950

atctgcaccc acctcccttg aaaaagagag aaaaaaaaa aaaaaaaa 1998

<210> 6
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80
 Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90
 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110
 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125
 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140
 Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160
 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175
 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190
 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220
 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255
 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270
 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285
 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300
 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320
 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335
 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350
 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 7

<211> 2119

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (205)..(1599)

<400> 7

acgttgacac aggaatgaag agtgtattgg ctgaatcttc aagcagaggc gatattgacc 60

atgtgctttt taaattggcc tgcgtgaccc gccacttgg tgtaaaagaa gaaccggcca 120

aaggggagggc ctgaaggacc tccacaggag tgtgagcagc actgcttcag caacaaagcc 180

tcagggtccac atcttgggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5

atg ctg atc ata gcc tgc gtt ggc agc act gtc ttc tac aga gaa cag 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25

cag acc tgg ttt gaa ggt gtc ttc ttg tct tcc atg tgc ccc att aat 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40

gtc agt gcc ggc acc ttt tat gga att atg ttt gat gcg ggc agc act 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55

gga gct cgg att cat gtt tac act ttt gtg cag aaa aca gca gga cag 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt 471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu
75 80 85

tct gct ttt gtg gat cag ccc aaa cag ggt gct gag act gtc cag gag 519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
90 95 100 105

ctc	ttg	gag	gtg	gcc	aaa	gac	tcg	atc	ccc	aga	agc	cac	tgg	gaa	agg	567
Leu	Leu	Glu	Val	Ala	Lys	Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Glu	Arg	
				110					115					120		
acc	ccg	gtg	gtt	ctg	aaa	gca	acg	gcc	gga	ctc	cgt	ttg	ctg	cct	gag	615
Thr	Pro	Val	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	
				125				130						135		
cag	aaa	gcc	cag	gct	ctg	ctc	ttg	gag	gta	gag	gag	atc	ttc	aag	aat	663
Gln	Lys	Ala	Gln	Ala	Leu	Leu	Leu	Glu	Val	Glu	Glu	Ile	Phe	Lys	Asn	
		140					145					150				
tca	cct	ttc	ctg	gtc	cca	gat	ggc	agc	ggt	agc	atc	atg	gat	ggg	tcc	711
Ser	Pro	Phe	Leu	Val	Pro	Asp	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	
		155				160					165					
tat	gaa	ggc	ata	cta	gcc	tgg	gtt	acc	gtg	aac	ttt	cta	aca	ggt	cag	759
Tyr	Glu	Gly	Ile	Leu	Ala	Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	
	170				175				180					185		
ctg	cat	ggt	cgt	ggc	cag	gag	act	gtg	ggg	acc	ctt	gac	ctg	ggg	ggt	807
Leu	His	Gly	Arg	Gly	Gln	Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	
			190					195						200		
gcc	tcc	acc	caa	atc	acg	ttt	cta	ccc	cag	ttt	gag	aaa	acc	ctg	gaa	855
Ala	Ser	Thr	Gln	Ile	Thr	Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	
			205					210					215			
caa	aca	cct	agg	ggc	tac	ctc	act	tcc	ttt	gag	atg	ttt	aac	agc	act	903
Gln	Thr	Pro	Arg	Gly	Tyr	Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	
		220					225					230				
ttt	aag	ctc	tat	aca	cat	agt	tac	ttg	gga	ttt	gga	ctg	aaa	gct	gca	951
Phe	Lys	Leu	Tyr	Thr	His	Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	
	235					240				245						
aga	ctg	gca	act	ctg	gga	gcc	ctg	gaa	gca	aaa	ggg	act	gat	gga	cat	999
Arg	Leu	Ala	Thr	Leu	Gly	Ala	Leu	Glu	Ala	Lys	Gly	Thr	Asp	Gly	His	
	250				255				260					265		
acg	ttt	cga	agt	gcc	tgt	tta	cca	aga	tgg	ttg	gaa	gca	gag	tgg	atc	1047
Thr	Phe	Arg	Ser	Ala	Cys	Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	
			270					275						280		
ttt	ggg	ggt	gtg	aaa	tac	cag	tat	ggt	ggt	aac	caa	gaa	ggg	gag	atg	1095
Phe	Gly	Gly	Val	Lys	Tyr	Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Val	Gln	Met	
			285				290						295			
ggc	ttt	gaa	ccc	tgc	tat	gcg	gaa	gtg	ctg	agg	gta	gta	cag	ggg	aaa	1143
Gly	Phe	Glu	Pro	Cys	Tyr	Ala	Glu	Val	Leu	Arg	Val	Val	Gln	Gly	Lys	
		300				305						310				
ctt	cac	cag	cca	gaa	gaa	gtc	cga	gga	agc	gcc	ttc	tac	gct	ttc	tct	1191
Leu	His	Gln	Pro	Glu	Glu	Val	Arg	Gly	Ser	Ala	Phe	Tyr	Ala	Phe	Ser	
		315				320					325					

tac tac tac gat cga gcc gct gac aca cac ttg atc gat tat gaa aag 1239
 Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys
 330 335 340 345

ggc ggg gtt tta aaa gtt gaa gat ttt gaa aga aaa gcc aga gaa gtg 1287
 Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val
 350 355 360

tgt gac aac ttg ggg agc ttc tcc tcg ggc agt cct ttc etc tgc atg 1335
 Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met
 365 370 375

gac etc act tac atc aca gcc ctg ttg aaa gat ggt ttg ggc ttt gcc 1383
 Asp Leu Thr Tyr Ile Thr Ala Leu Lys Asp Gly Leu Gly Phe Ala
 380 385 390

gaa cgg cac cct ctt aca gct cac aaa gaa agt gaa caa cat aga gac 1431
 Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp
 395 400 405

tgg ttg ggc ctt ggg ggc cac ctt tca cct gct cca gtc tct ggg cat 1479
 Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His
 410 415 420 425

cac cag ctg agg cca agc tcc acc tct gaa gcc tgc att tct gaa cca 1527
 His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro
 430 435 440

gtt ttc tca cag gaa ggc gtg gac tca gag aca ttt tct gac etc tct 1575
 Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser
 445 450 455

gga aaa gcc tgg ccc gaa acc cgt taactgggtt tataaggagg gaggggtttt 1629
 Gly Lys Ala Trp Pro Glu Thr Arg
 460 465

tagatgagtc ttgctcttga gcctagtgat ttgggcttca atgatttgca catctaattg 1689

gaatagctcc taaccacttg gtgggtgcat ggctggcacc agactgtaaa tcttttggga 1749

ttctttgtac agagtcctcg aaaggaaaaa agagaaaaagg ttggaactc catgctagat 1809

tgcgagtcca gagacaggtc cctggggacc aaagaacaat ctggtttcaa cccttggtg 1869

cctcattgct ttgaatggat tcatttttgc ttataagctg atttactgaa atcccataac 1929

ccatcaatgc tgtaattttt ttcttctcta cccttattac attccctacc ctaaaagcct 1989

gggggaaata cctgggtttg ctcccatctc ataattgaga aagagggggg aaaagatact 2049

gtattagaat ttgtgtgate ctgtggcaca atagatcaac caacccattt aaagcttaaa 2109

aaaaaaaaaa 2119

<210> 8
 <211> 465
 <212> PRT

<213> Mus musculus

<400> 8

```

Met Ala Thr Ser Trp Gly Ala Val Phe Met Leu Ile Ile Ala Cys Val
 1           5           10           15

Gly Ser Thr Val Phe Tyr Arg Glu Gln Gln Thr Trp Phe Glu Gly Val
          20           25           30

Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr
          35           40           45

Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
          50           55           60

Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
          65           70           75           80

Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
          85           90           95

Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
          100          105          110

Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
          115          120          125

Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
          130          135          140

Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
          145          150          155          160

Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
          165          170          175

Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
          180          185          190

Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
          195          200          205

Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
          210          215          220

Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
          225          230          235          240

Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
          245          250          255

Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
          260          265          270

Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
          275          280          285

```

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
290 295 300

Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
305 310 315 320

Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
325 330 335

Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
340 345 350

Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
355 360 365

Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
370 375 380

Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
385 390 395 400

His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
405 410 415

Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
420 425 430

Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val
435 440 445

Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr
450 455 460

Arg
465

<210> 9

<211> 428

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95
 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110
 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125
 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140
 Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160
 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175
 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190
 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220
 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255
 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270
 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285
 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300
 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320
 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335
 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350
 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365
 Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
 370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 10

<211> 455

<212> PRT

<213> P. sativum

<400> 10

Met Glu Leu Leu Ile Lys Leu Ile Thr Phe Leu Leu Phe Ser Met Pro
1 5 10 15

Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn Leu Leu Thr Ser Arg
20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
210 215 220

Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val
 225 230 235 240
 His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu
 245 250 255
 Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn
 260 265 270
 Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr
 275 280 285
 Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu
 290 295 300
 Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile
 305 310 315 320
 Trp Asn Gly Gly Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser
 325 330 335
 Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr
 340 345 350
 Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu
 355 360 365
 Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu
 370 375 380
 Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln
 385 390 395 400
 Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile
 405 410 415
 Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala
 420 425 430
 Trp Pro Leu Gly Asn Ala Val Glu Ala Ile Ser Ala Leu Pro Lys Phe
 435 440 445
 Glu Arg Leu Met Tyr Phe Val
 450 455

<210> 11

<211> 454

<212> PRT

<213> Solanum tuberosum

<400> 11

Met Leu Asn Gln Asn Ser His Phe Ile Phe Ile Ile Leu Ala Ile Phe
 1 5 10 15

Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile
 20 25 30

Pro Leu Arg Arg His Leu Leu Ser His Glu Ser Glu His Tyr Ala Val
 35 40 45
 Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Phe Arg Phe
 50 55 60
 Asp Glu Lys Leu Gly Leu Leu Pro Ile Gly Asn Asn Ile Glu Tyr Phe
 65 70 75 80
 Met Ala Thr Glu Pro Gly Leu Ser Ser Tyr Ala Glu Asp Pro Lys Ala
 85 90 95
 Ala Ala Asn Ser Leu Glu Pro Leu Leu Asp Gly Ala Glu Gly Val Val
 100 105 110
 Pro Gln Glu Leu Gln Ser Glu Thr Pro Leu Glu Leu Gly Ala Thr Ala
 115 120 125
 Gly Leu Arg Met Leu Lys Gly Asp Ala Ala Glu Lys Ile Leu Gln Ala
 130 135 140
 Val Arg Asn Leu Val Lys Asn Gln Ser Thr Phe His Ser Lys Asp Gln
 145 150 155 160
 Trp Val Thr Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Met Trp Ala
 165 170 175
 Ala Ile Asn Tyr Leu Leu Gly Asn Leu Gly Lys Asp Tyr Lys Ser Thr
 180 185 190
 Thr Ala Thr Ile Asp Leu Gly Gly Ser Val Gln Met Ala Tyr Ala
 195 200 205
 Ile Ser Asn Glu Gln Phe Ala Lys Ala Pro Gln Asn Glu Asp Gly Glu
 210 215 220
 Pro Tyr Val Gln Gln Lys His Leu Met Ser Lys Asp Tyr Asn Leu Tyr
 225 230 235 240
 Val His Ser Tyr Leu Asn Tyr Gly Gln Leu Ala Gly Arg Ala Glu Ile
 245 250 255
 Phe Lys Ala Ser Arg Asn Glu Ser Asn Pro Cys Ala Leu Glu Gly Cys
 260 265 270
 Asp Gly Tyr Tyr Ser Tyr Gly Gly Val Asp Tyr Lys Val Lys Ala Pro
 275 280 285
 Lys Lys Gly Ser Ser Trp Lys Arg Cys Arg Arg Leu Thr Arg His Ala
 290 295 300
 Leu Lys Ile Asn Ala Lys Cys Asn Ile Glu Glu Cys Thr Phe Asn Gly
 305 310 315 320
 Val Trp Asn Gly Gly Gly Gly Asp Gly Gln Lys Asn Ile His Ala Ser
 325 330 335

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
340 345 350

Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
355 360 365

Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
370 375 380

Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
385 390 395 400

Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
405 410 415

Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
420 425 430

Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
435 440 445

Ile Arg Val Ala Ser Ser
450

<210> 12

<211> 473

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
1 5 10 15

Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
20 25 30

Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
35 40 45

Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
50 55 60

Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
65 70 75 80

Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
85 90 95

Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
100 105 110

Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
115 120 125

Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly
 145 150 155 160
 Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp
 165 170 175
 Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys
 180 185 190
 Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Gly Ser Thr Gln Ile
 195 200 205
 Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu
 210 215 220
 His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln
 225 230 235 240
 Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn
 245 250 255
 Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys
 260 265 270
 Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val
 275 280 285
 Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr
 290 295 300
 Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe
 305 310 315 320
 Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro
 325 330 335
 Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys
 340 345 350
 Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr
 355 360 365
 Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp
 370 375 380
 Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe
 385 390 395 400
 Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe
 405 410 415
 Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp
 420 425 430
 Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys
 435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
 450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
 465 470

<210> 13
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 13
 Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
 1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
 20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
 35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
 50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
 65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
 85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
 100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
 115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
 130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
 145 150

<210> 14
 <211> 154
 <212> PRT
 <213> Rattus norvegicus

<400> 14
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
 1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
 35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Arg Met Glu Ser Lys
85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
145 150

<210> 15
<211> 153
<212> PRT
<213> Homo sapiens

<400> 15
Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16
 <211> 150
 <212> PRT
 <213> Gallus gallus

<400> 16
 Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val
 1 5 10 15
 Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val
 20 25 30
 Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr
 35 40 45
 Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser
 50 55 60
 Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu
 65 70 75 80
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro
 85 90 95
 Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr
 100 105 110
 Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Glu Gly
 115 120 125
 Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
 130 135 140
 Arg Gly Trp Leu Gly Glu
 145 150

<210> 17
 <211> 148
 <212> PRT
 <213> Caenorhabditis elegans

<400> 17
 Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu
 1 5 10 15
 Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp
 20 25 30
 Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly
 35 40 45
 Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr
 50 55 60
 Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly
 65 70 75 80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
130 135 140

Gly Arg Phe Asp
145

<210> 18
<211> 10
<212> RNA
<213> Mus musculus

<400> 18
aagaauagg 10

<210> 19
<211> 10
<212> RNA
<213> Vertebrate

<400> 19
gccgccagg 10

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ccagactgta aatcttttgg 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
agggaatgta ataagggtag 20

<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 22
 ctgcttgagt gacgtctctg 20

 <210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 23
 cacatgaggt tcagctctgtg 20

 <210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 24
 gtgaagtggc tgccttcagg 20

 <210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 25
 cctttgactc gggactccag 20

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 26
 gaactgctgc ctaaccactc 20

<210> 27
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 27
 attgatgggt cttgggattg c 21

<210> 28
 <211> 10
 <212> RNA
 <213> Homo sapiens

<400> 28
 augugaauga 10

<210> 29
 <211> 10
 <212> RNA
 <213> Homo sapiens

<400> 29
 acaagggauga 10